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LOCUS       MAU18263                1665 bp    DNA     linear   BCT 26-OCT-1995
DEFINITION  Mycobacterium avium alkyl hydroperoxidase C (ahpC) gene, complete
            cds, and OxyR homolog gene, complete cds.
ACCESSION   U18263
VERSION     U18263.1  GI:1040852
SOURCE      Mycobacterium avium
  ORGANISM  Mycobacterium avium
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            avium complex (MAC).
REFERENCE   1  (bases 1 to 1665)
  AUTHORS   Sherman,D.R., Sabo,P.J., Hickey,M.J., Arain,T.M., Mahairas,G.G.,
            Yuan,Y., Barry,C.E. III and Stover,C.K.
  TITLE     Disparate responses to oxidative stress in saprophytic and
            pathogenic mycobacteria
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6625-6629 (1995)
REFERENCE   2  (bases 1 to 771)
  AUTHORS   Yamaguchi,R., Matsuo,K., Yamazaki,A., Takahashi,M., Fukasawa,Y.,
            Wada,M. and Abe,C.
  TITLE     Cloning and expression of the gene for the Avi-3 antigen of
            Mycobacterium avium and mapping of its epitopes
  JOURNAL   Infect. Immun. 60 (3), 1210-1216 (1992)
REFERENCE   3  (bases 1 to 1665)
  AUTHORS   Hickey,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-DEC-1994) Mark J. Hickey, TB & Molecular
            Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA
            98119, USA
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Query Match              14.1%;  Score 235.8;  DB 1;  Length 1665;
Best Local Similarity    55.3%;  Pred. No. 5.7e-48;
Matches  506;  Conservative    0;  Mismatches  397;  Indels   12;  Gaps    2;
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Qy    469 ATTCACCGTTATAGTTATAGGCATGAGCAATAAAGAGTACCGGCCCACACTCGCCCAGCT 528
          |||  ||  || | ||||||| |||  | ||||    || | |||||| ||||||   ||
Db    682 ATTTCCCACTACACTTATAGGTATGCCCGATAAGACTTATCAGCCCACGATCGCCGGCCT 741


Qy    529 TCGCACCTTTGTCACCATCGCAGAATGCAAGCACTTTGGTACTGCTGCCACCAAGCTGTC 588
          ||| |||| |||  |  |||| ||        || ||  |   ||| || ||      ||
Db    742 GCGCGCCTTCGTCGCGGTCGCCGAGAAGCGCCAATTCAGCGGTGCCGCAACGGCTTTGGG 801


Qy    589 CATTTCGCAGCCATCCCTCTCCCAGGCACTTGTCGCATTAGAAACAGGCCTGGGAGTTCA 648
          |    ||| |  | | || || |||| | |  ||  | || | || ||·|||||||   ||
Db    802 AGTCAGCCAGTCGACGCTGTCGCAGGTGTTGGCGGCGCTGGAGGCGGGGCTGGGCACGCA 861


Qy    649 GCTGATTGAACGCTCCACCCGCAAGGTCATTGTCACCCCAGCGGGCGAGAAGTTGCTGCC 708
          | || | || |||||||||| |    ||| | | || ||   ||||| || ||||||.||
Db    862 GTTGGTGGAGCGCTCCACCCGGCGTGTCTTCTTGACACCCCAGGGCGCCGAGCTGCTGCC 921


Qy    709 ATTCGCCAAATCCACCCTTGACGCGGCGGAGTCTTTCCTCTCCCACGCCAAGGGCGCCAA 768
          |||| |  ||  | || |||||| || | ||| ||    ||   ||| ||  ||| | |
Db    922 GCACGCCCAGGCCGTGGTCGAGGCGGCCGACGCCTTCACCGCGGCGGCGGCGGGTTCGAC 981


Qy    769 CGGTTCGCTCACTGGACCGTTGACCGTAGGCATCATCCCCACGGCGGCTCCTTACATTTT 828
          |   ||| |     | |    ||   | ||| | || |||||||||| || || ||| | |
Db    982 GGACCCGTTGCGGGCCGGCATGCGGCTGGGGCTGATCCCCACGGTGGTGCCCTACGTGCT 1041
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Qy    ·829  GCCGTCAATGCTGTCCATCGTGGATGAAGAATATCCAGATCTGGAACCTCACATCGTCGA  888
            ||||  |  ||||||  ||    |  |   |||           ||  |  |||   |  |   ||   |||
Db    1042  GCCGACCGTGCTGGCCGGAATCGCCGAACGGCGGCCCGGCCTGACCCTGCGGGTCACCGA  1101

Qy     889  GGACCAAACCAAGCATCTTCTCGCGTTGCTGCGCGACGGCGCCATCGACGTCGCCATGAT  948
            ||||||  |||  |  |   ||  ||  |||  ||||||||||  ||||||  ||||||  ||   ||||
Db    1102  GGACCAGACCGAACGGCTGCTGGCGGTGCTGCGCGAGGGCGCCCTCGACGCGGCGCTGAT  1161

Qy     949  GGCCCTGCCTTCTGAGGCACCAGGCATGAAGGAAATCCCCCTCTACGACGAAGACTTTAT  1008
            ||  |||||   |  |||  |   |  |  |||   |  |   |   |||||   |||||||||||   ||  ||   |
Db    1162  CGCGCTGCCCGCCGAGACGGCGGGCGTCACCGCGATCCCGATCTACGACGAGGATTTCGT  1221

Qy    1009  CGTCGTTACAGCTAGCGATCACCCCTTCGCCGGCCGCCAAGACTTAGAACTATCCGCCTT  1068
            |||·    |     |    ||||||  |  ||  |||    |           |   |||  |
Db    1222  GCTCGCGCTTCCGCCGGGCCACCCGCTGGCGGGCAAGCGCCGGGTGCCGGCGACGGCGCT  1281

Qy    1069  AGAAGACCTCGATCTGCTGCTTCTCGACGACGGACACTGCCTCCACGACCAAATTGTGGA  1128
            |  |||||      |||||||||  ||  |||||||  ||  |||||||||  |  ||||||         ||||
Db    1282  GGCCGACCTGCCGCTGCTGCTGCTGGACGAGGGGCACTGCCTGCGCGACCAGGCGCTGGA  1341

Qy    1129 ·CCTGTGCCGCCGCGGAGACATCAACCCCATTAGCTCCACTACTGCTGTCACCCGCGCATC  1188
            | | ||||| |   |·| | |   |   |         |||  |   ·|||||  ||   |
Db    1342  CGTCTGCCACAAGGCGGGTGTGCGGGCGGAGCTGGCCAAT---------ACCCGGGCCGC  1392

Qy    1189  CAGCCTTACCACCGTCATGCAGCTCGTCGTCGCCGGCCTTGGATCCACCTTGGTCCCAAT  1248
            |    ||   ||||||·     |||||   |||    ||  |||||||  ||   ||  |  |  ||||
Db    1393  CTCGCTGGCCACCGCGGTGCAGTGCGTGACCGGCGGCCTGGGGGTGACGCTCATCCCGCA  1452

Qy    1249  CAGCGCAATCCCATGGGAATGCACCCGACCAGGACTGGCAACAGCCAACTTCAACTCTGA  1308
            ·|||||  ||||   |||      | ||      | ||||   |||  |  |||  |  |  |
Db    1453  GAGCGCGGTCCCGGTGGAGGCGTCGCGCAGCCGGCTGGGCCTGGCCCAGTTCGCCGCGCC  1512

Qy    1309  TGTCACCGCAAACCGCCGCATTGGATTGGTGTACCGTTCCTCTTCTTCTCGCGCCGAAGA  1368
            | | |         |||  |||||  ||·||||||  |||  ||  ||        |||| |||
Db    1513  GCGCCCGG---GCCGGCGCATCGGCCTGGTGTTCCGCTCGTCGAGCGGGCGCGACGACTC  1569

Qy    1369  GTTCGAACAGTTTGC  1383
            |  |     ||  |  ||
Db    1570  CTACCGCGAGCTGGC  1584
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